**Figure 1:** Restriction pattern of the HAL coding region cut with selected enzymes.
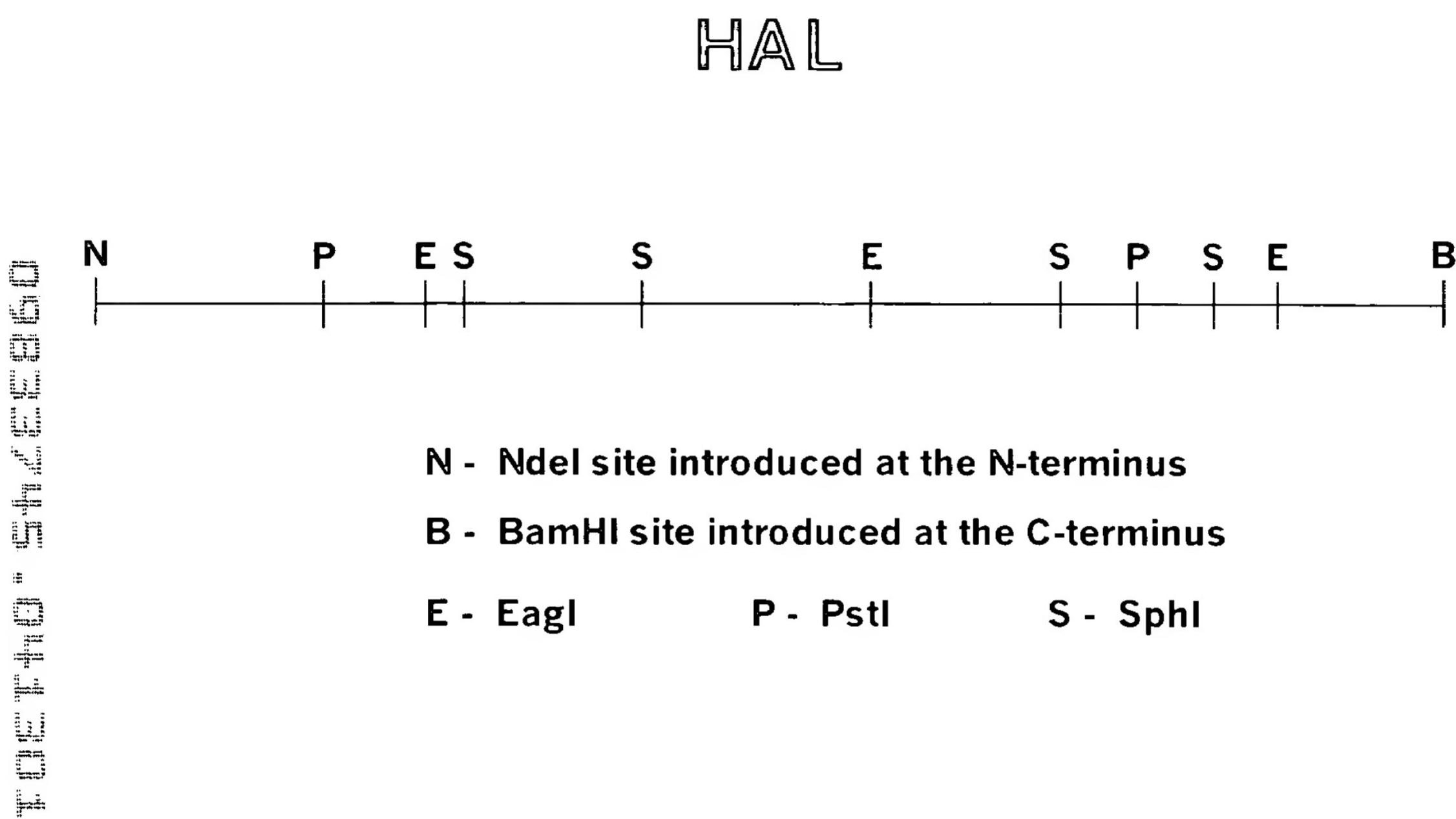
HAL

N - Ndel site introduced at the N-terminus

B - BamHI site introduced at the C-terminus

E - EagI   P - PstI   S - SphI

002.565804.1

Figure 2: Experimentally derived peptide sequences of HAL

N-terminal

      (M)ASAPQITLGLSGATAD

Internal

      (M)ALADLDELLDEA

      (M)GEPVEREVLRA

Figure 3: SphI digestion pattern of HAL gene showing oligonucleotide and subclones.
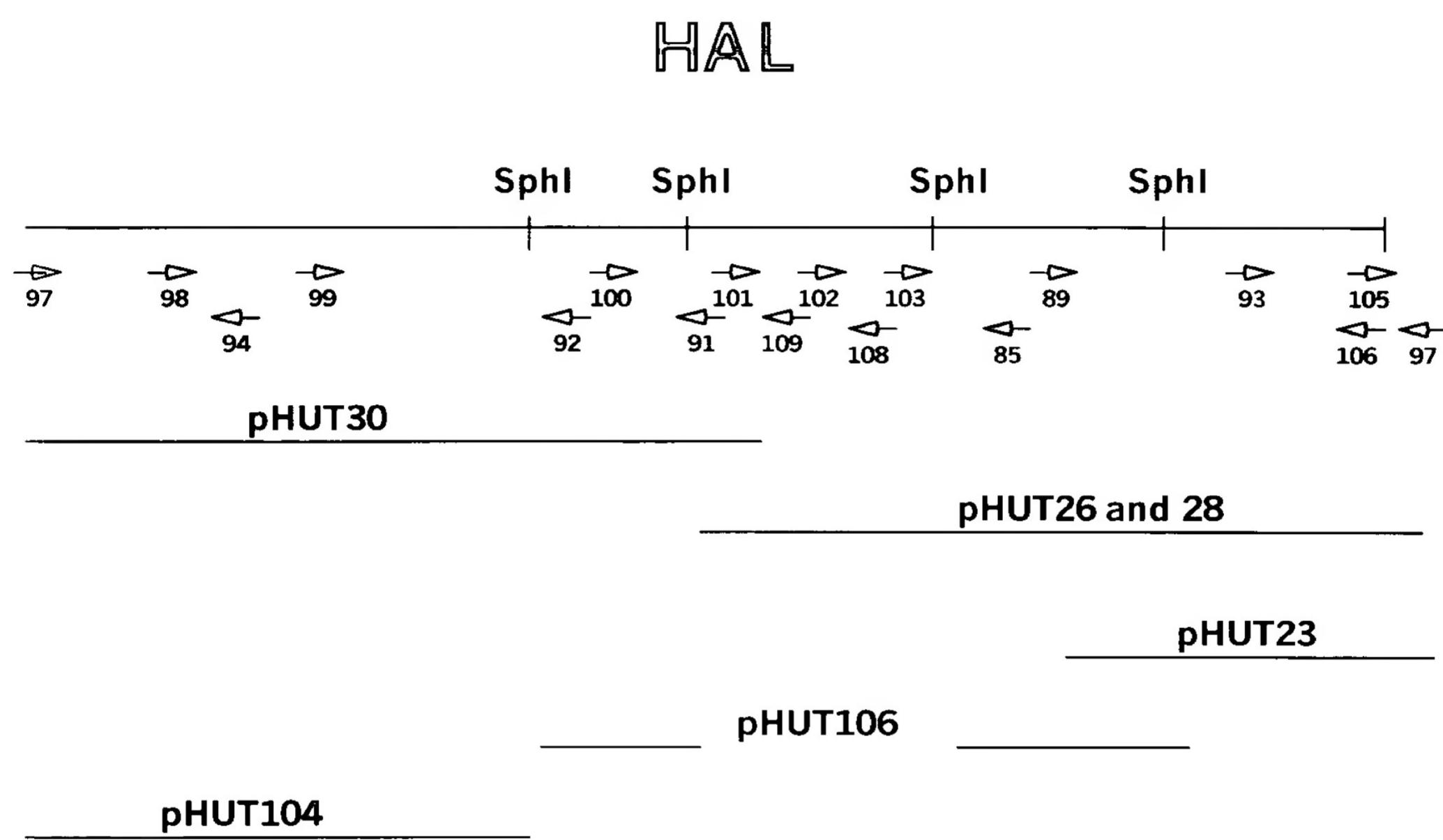
Figure 4: Histidine ammonia lyase overexpressing plasmid.
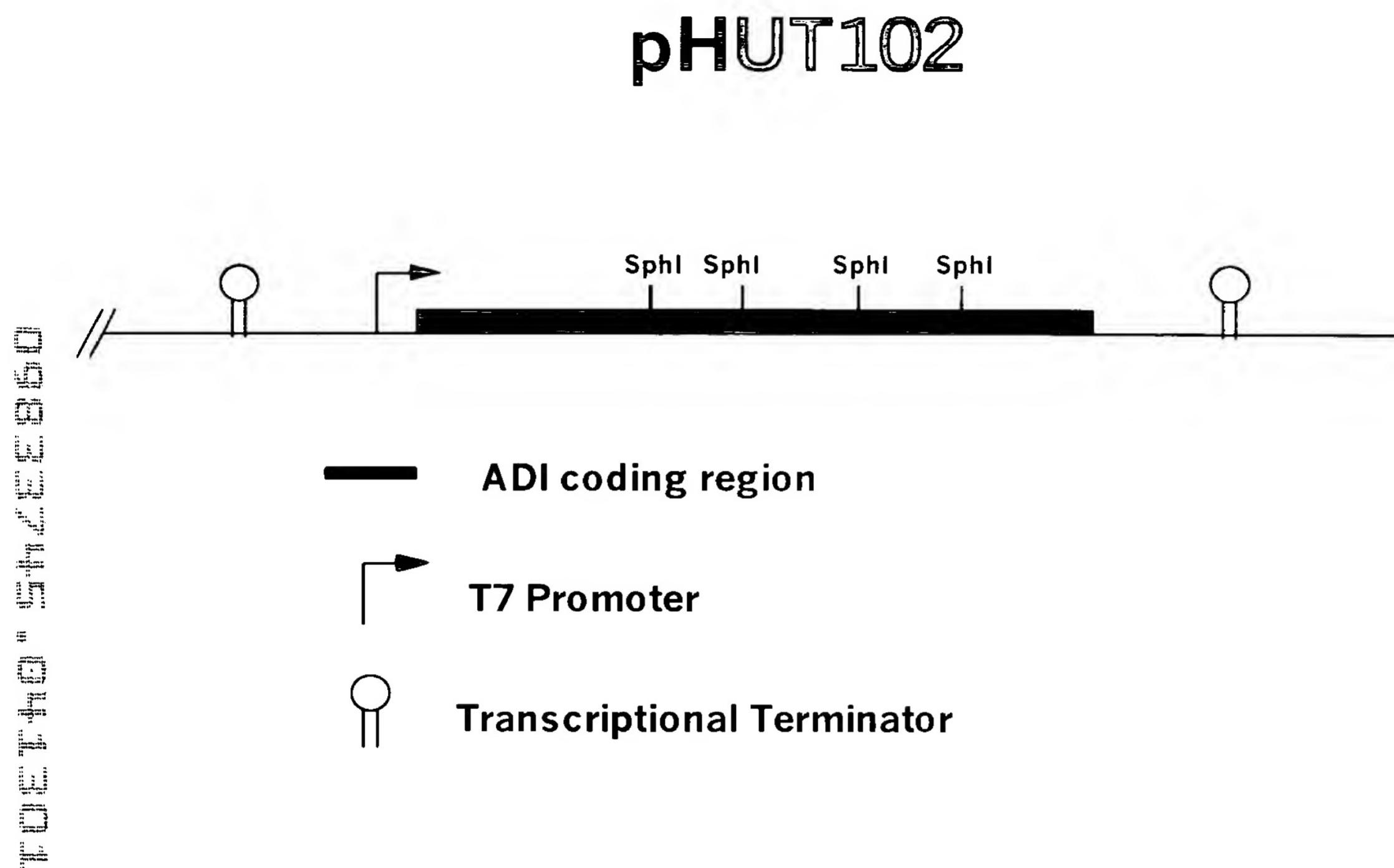
pHUT102

Sphl   Sphl   Sphl   Sphl

━━━ ADI coding region

T7 Promoter

Transcriptional Terminator

Figure 5: SDS-PAGE showing expression of HAL in *E. coli*.
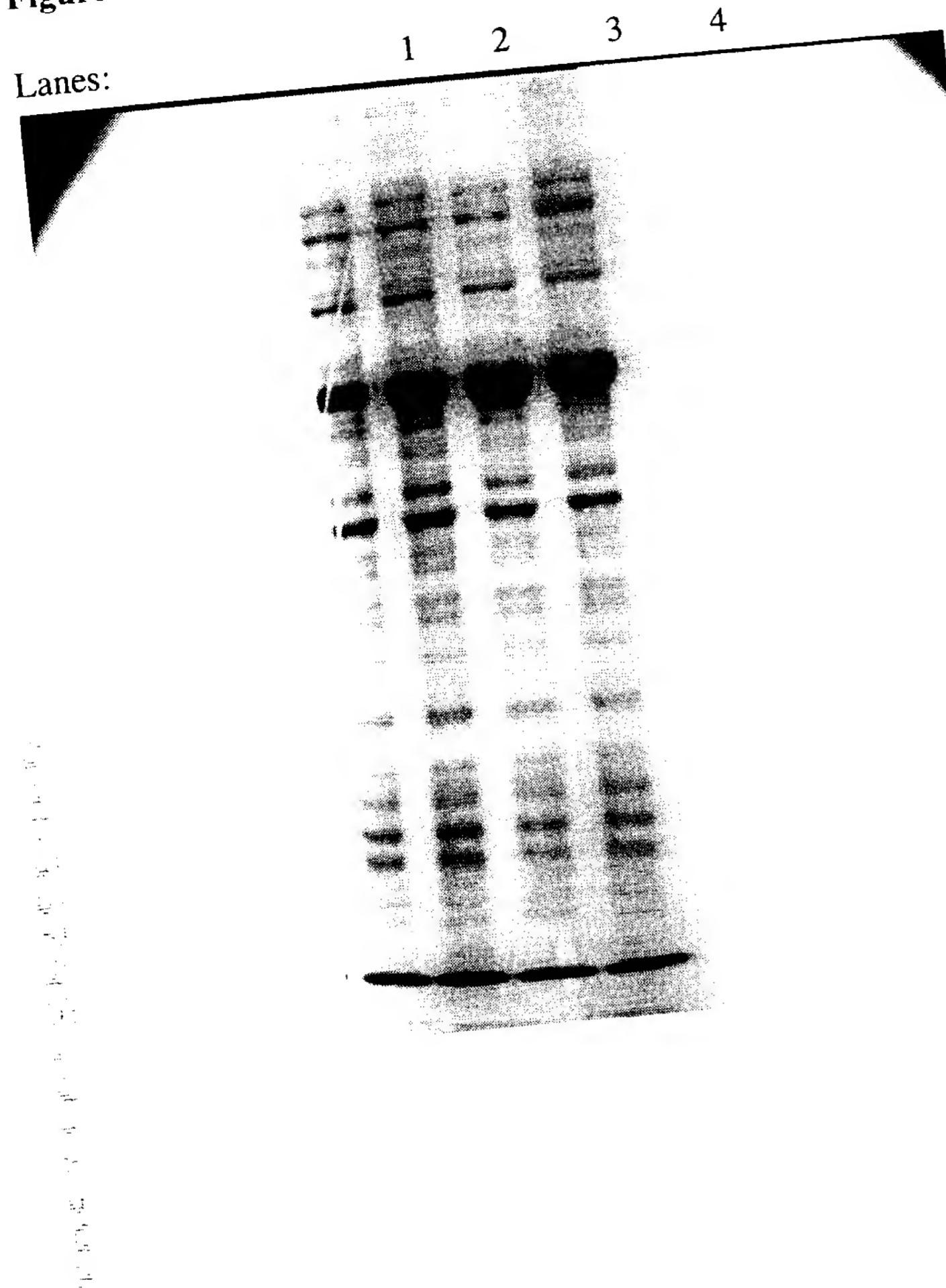
Lanes:

Figure 6: SDS-PAGE showing purification of HAL from *E. coli*
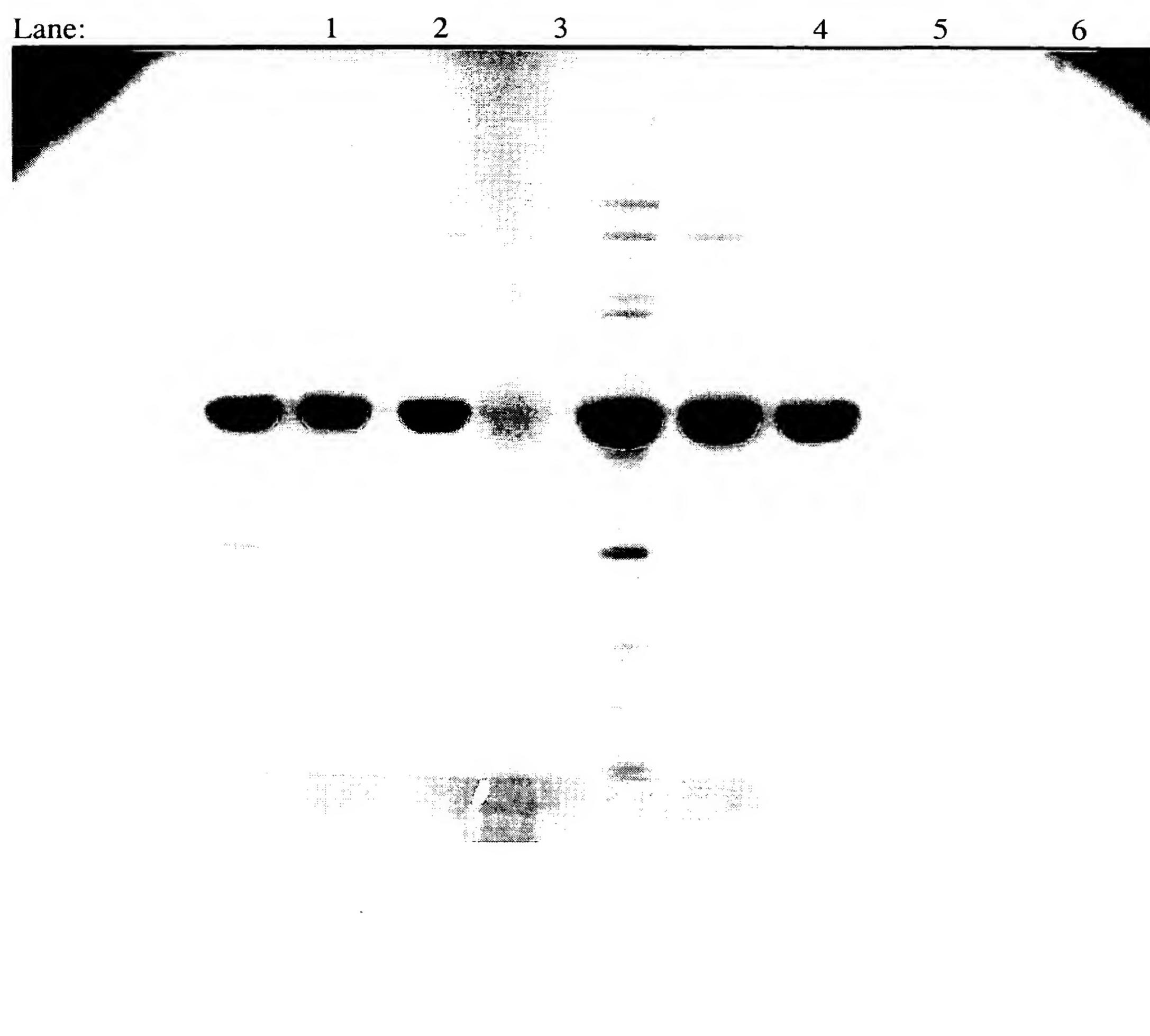
Figure 7: Effect of Temperature on HAL
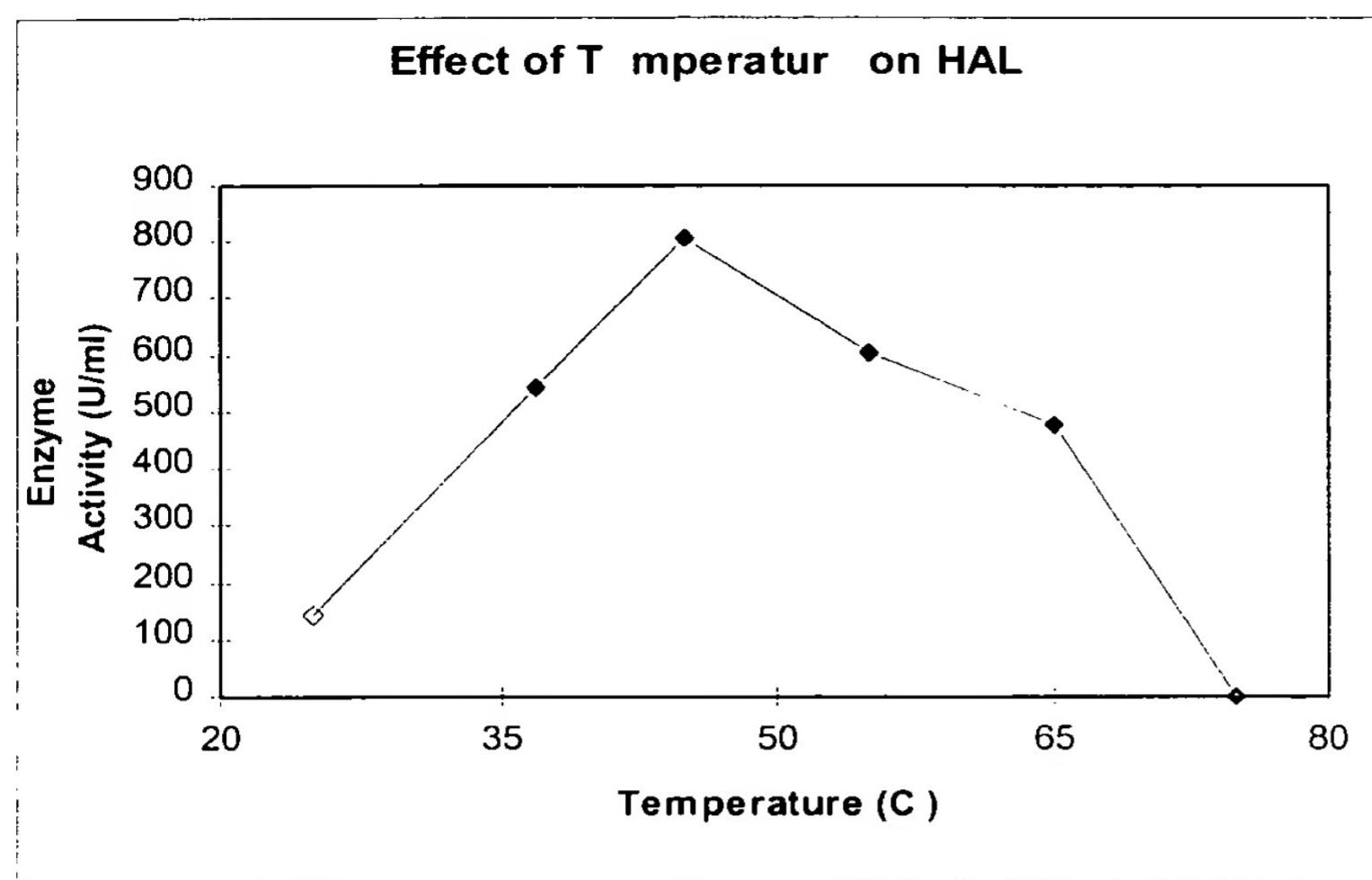
Effect of T mperatur on HAL

Figure 8: Effect of pH on HAL.

Figure 9: Effect of HAL and Histidinol on HSV.
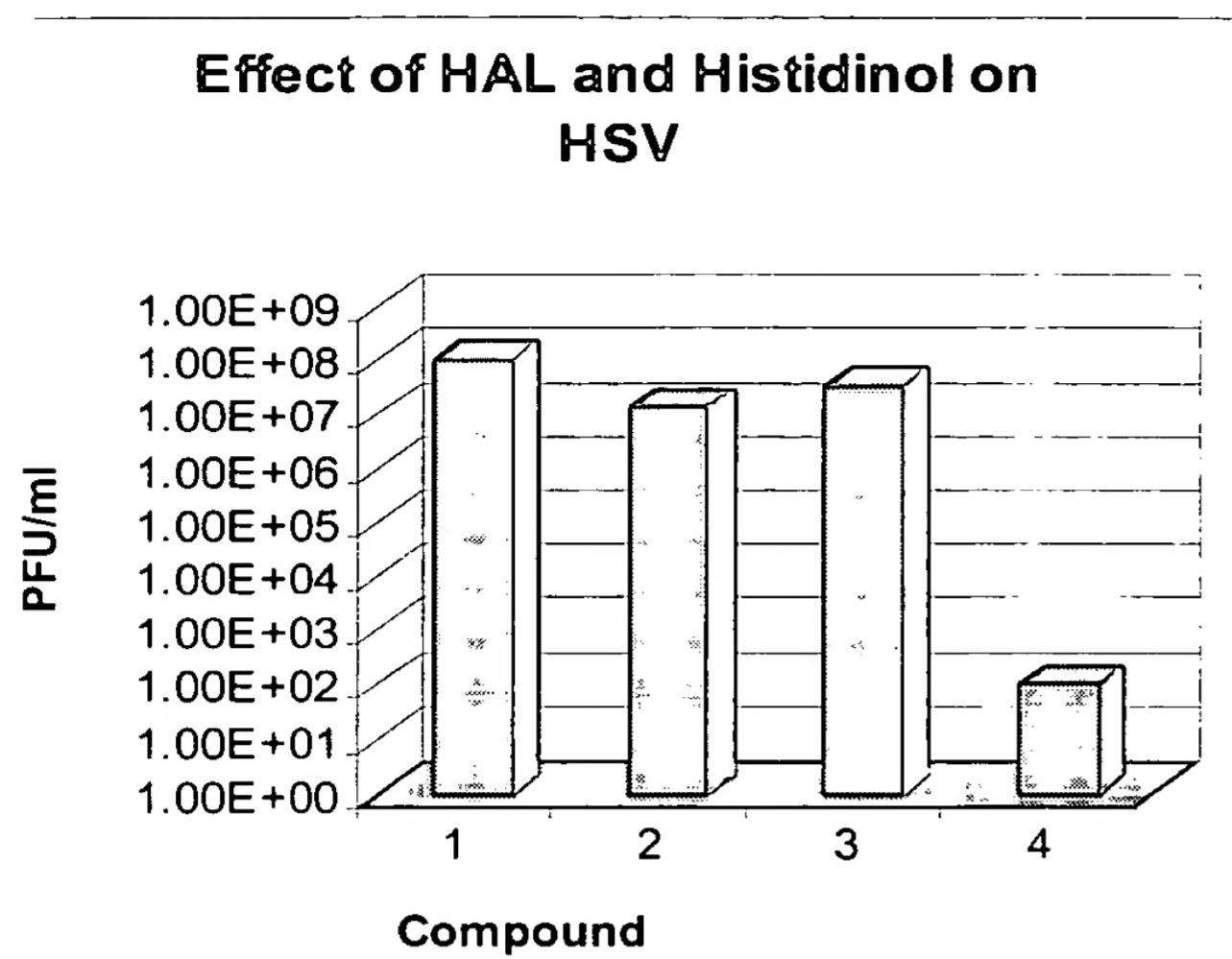
Effect of HAL and Histidinol on HSV

Figure 10: Effectiveness of L-histidinol as a Single Agent
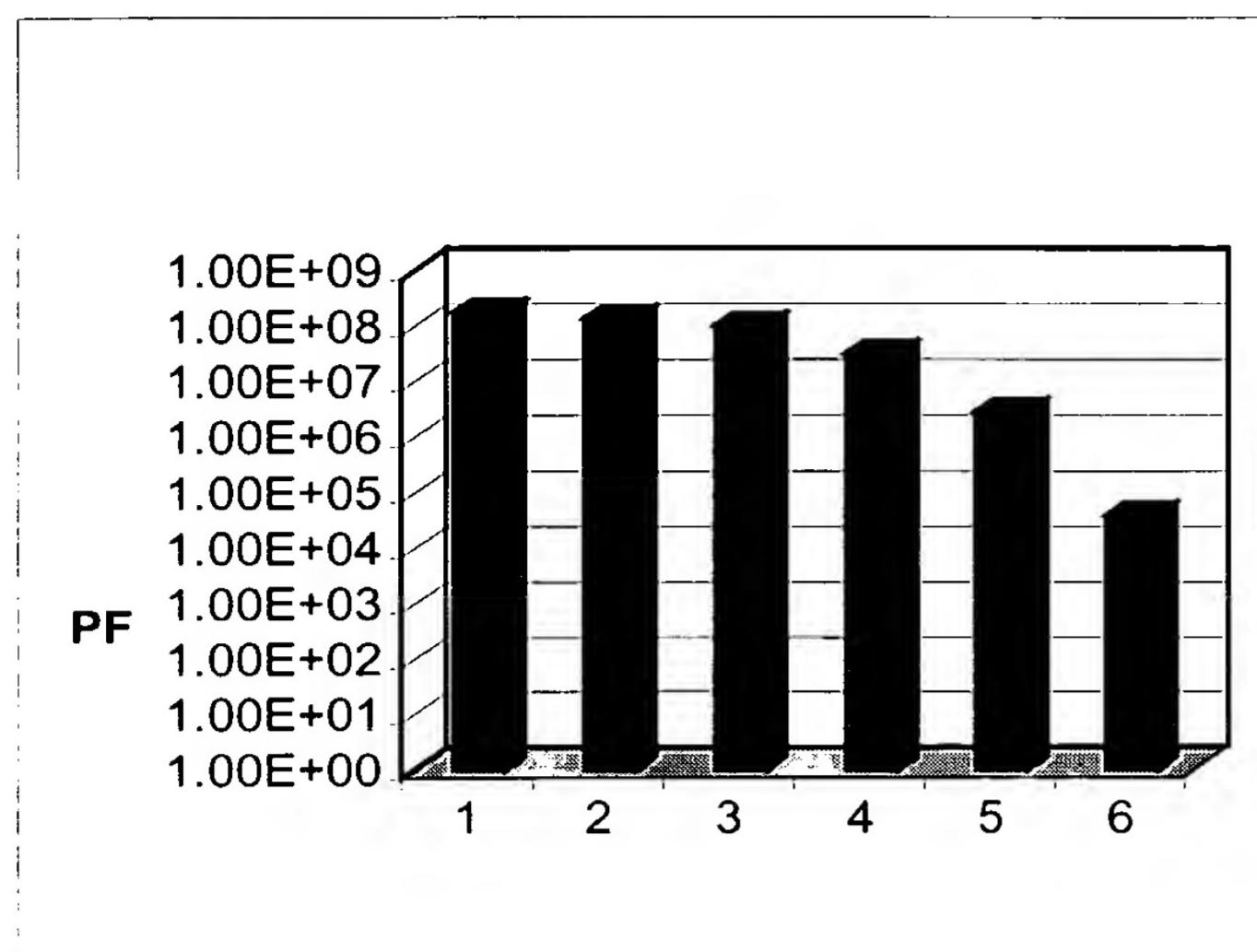
Figure 11: Effect of HAL and Histidinol on RSV.
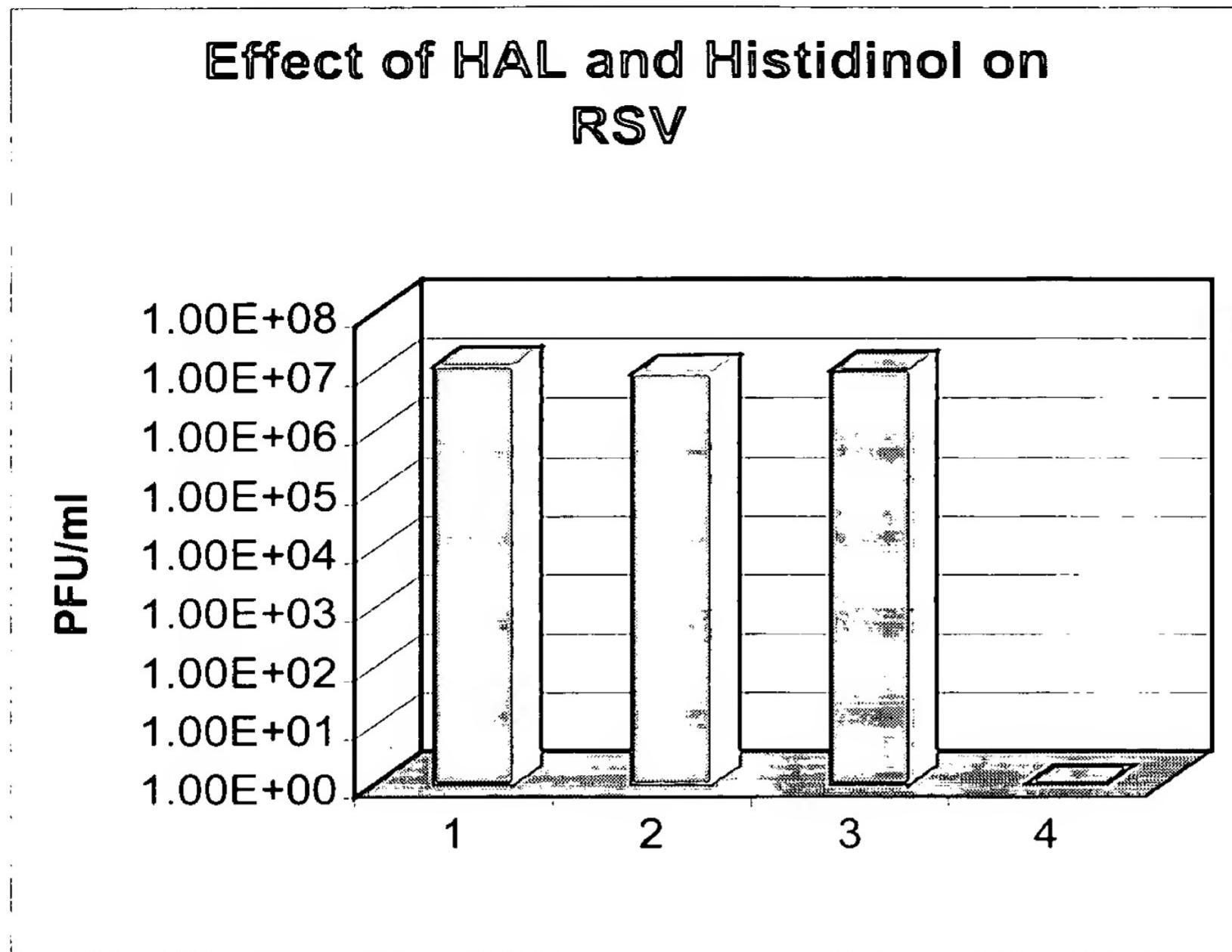
Effect of HAL and Histidinol on RSV

Figure 12: Effect of HAL on RMuLV.

Effect of HAL on RMuLV
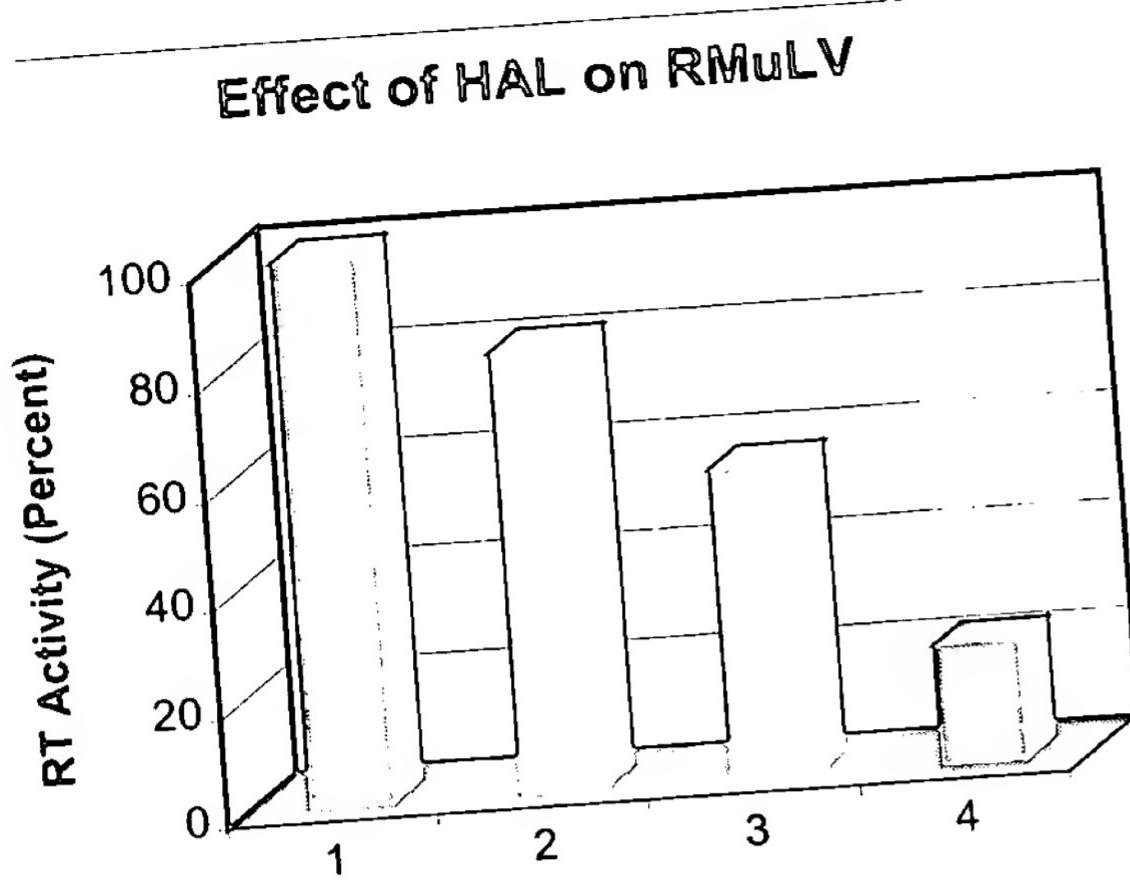
Figure 13: Histidine ammonia lyase peptide sequence pileup

```
HUTH_PSEPU      -------------------------------------------------------
-

HUTH_RHIME      -------------------------------------------------------
-

HUTH_MOUSE
MPRYTVHVRGEWLAVPCQDGKLTVGWLGREAVRRYMKNKPDNGGFTSVDEVQFLVHRCKG
HUTH_RAT
MPRYTVHVRGEWLAVPCQDGKLSVGWLGREAVRRYMKNKPDNGGFTSVDEVRFLVRRCKG
HUTH_HUMAN
MPRYTVHVRGEWLAVPCQDAQLTVGWLGREAVRRYIKNKPDNGGFTSVDDAHFLVRRCKG
HUTH_CAEEL      -MRLQVQIGTECVVVPCKP-DDTIHAVAKKSVEKLRRLRPK----
LPLADDYFEVRRTVG
HUTH_BACS       -------------------------------------------------------
-

HUTH_STRGR      -------------------------------------------------------
-

HUTH_CORY       -------------------------------------------------------
-


HUTH_PSEPU      -------------------------------------------------------
-

HUTH_RHIME      -------------------------------------------------------
-

HUTH_MOUSE      LGLLDNEDELEVALEDNEFVEVVIEGDVMS-------PDFIPSQPEGVFLYSKYR---
-

HUTH_RAT        LGLLDNEDLLEVALEDNEFVEVVIEGDVMS-------PDFIPSQPEGVFLYSKYR---
-

HUTH_HUMAN      LGLLDNEDRLEVALENNEFVEVVIEGDAMS-------PDFIPSQPEGVYLYSKYR---

HUTH_CAEEL
NSLLDPEDLVSDVLKDSDFIIVAASVEETEDAKEAKKQEEIDNARAEIEKIDNRRRKVSF
HUTH_BACS       -------------------------------------------------------
-

HUTH_STRGR      -------------------------------------------------------
-

HUTH_CORY       -------------------------------------------------------
-


HUTH_PSEPU      -------------
TELTLKPGTLTLAQLRAIHAAPVRLQLDASAAPAIDASVACVEQIIA
HUTH_RHIME      -------------
MTVILRPGSVPLSDLETIYWTGAPARLDAAFDAGIAKAAARIAEIVA
HUTH_MOUSE      ----------
EPEKYIALDGDSLSTEDLVNLGKGRYKIKLTSIAEKKVQQSREVIDSIIK
HUTH_RAT        ----------
EPEKYIALDGDSLSTEDLVNLGKGHYKIKLTSIAEKKVQQSREVIDSIIK
HUTH_HUMAN      ----------
EPEKYIELDGDRLTTEDLVNLGKGRYKIKLTPTAEKRVQKSREVIDSIIK
HUTH_CAEEL
ADSLAPMVLAPPTKLLILDGNSLLPEDLVRCEKGECAIQLSMESEDRIRKARTFLEKIAS
HUTH_BACS       --------------
MVTLDGSSLTTADVARVLFDFEEAAASEESMERVKKSRAAVERIVR
HUTH_STRGR      ----------
MDMHTVVVGTSGTTAEDVVAVARHGARVELSAAAVEALAAARLIVDALAA
HUTH_CORY       ---------
MASAPQITLGLSGATADDVIAVARHEARISISPQVLEELASVRAHIDALAS
```

Figure 13 cont'd.

```
HUTH_PSEPU
EDRTAYGINTGFGLLASTRIASHDLENLQRSLVLSHAAGIGAPLDDDLVRLIMVLKINSL
HUTH_RHIME
GNAPVYGINTGFGKLASIKIDSSDVATLQRNLILSHCCGVGQPLTEDIVRLIMALKLISL
HUTH_MOUSE
ERTVVYGITTGFGKFARTVIPANKLQELQVNLVRSHSSGVGKPLSPERCRMLLALRINVL
HUTH_RAT
ERTVVYGITTGFGKFARTVIPANKLQELQVNLVRSHSSGVGKPLSPERCRMLLALRINVL
HUTH_HUMAN
EKTVVYGITTGFGKFARTVIPINKLQELQVNLVRSHSSGVGKPLSPERCRMLLALRINIL
HUTH_CAEEL
EHRAVYGVTTGFGTFSNVTIPPEKLKKLQLNLIRSHATGYGEPLAPNRARMLLALRINIL
HUTH_BACS
DEKTIYGINTGFGKFSDVLIQKEDSAALQLNLILSHACGVGDPFPECVSRAMLLLRANAL
HUTH_STRGR
KPEPVYGVSTGFGALASRHIGTELRAQLQRNIVRSHAAGMGPRVEREVVRALMFLRLKTV
HUTH_CORY
ADTPVYGISTGFGALATRHIAPEDRAKLQRSLIRSHAAGMGEPVEREVVRALMFLRAKTL


HUTH_PSEPU
SRGFSGIRRKVIDALIALVNAEVYPHIPLKGSVGASGDLAPLATMSLVLLGEGKARYKGQ
HUTH_RHIME
GRGASGVRLELVRLIEAMLDKGVIPLIPEKGSVGASGDLAPLAHMAAVMMGHGEAFFAGE
HUTH_MOUSE
AKGYSGISLETLKQVIEAFNASCLSYVPEKGTVGASGDLAPLSHLALGLIGEGKMWSPKS
HUTH_RAT
AKGYSGISLETLKQVIEVFNASCLSYVPEKGTVGASGDLAPLSHLALGLIGEGKMWSPKS
HUTH_HUMAN
AKGYSGISLETLKQVIEMFNASCLPYVPEKGTVGASGDLAPLSHLALGLVGEGKMWSPKS
HUTH_CAEEL
AKGHSGISVENIKKMIAAFNAFCVSYVPQQGTVGCSGDLCPLAHLALGLLGEGKMWSPTT
HUTH_BACS
LKGFSGVRAELIEQLLAFLNKRVHPVIPQQGSLGASGDLAPLSHLALALIGQGEVFFEGE
HUTH_STRGR
ASGHTGVRPEVAQTMADVLNAGITPVVHEYGSLGCSGDLAPLSHCALTLMGEGEAEGPDG
HUTH_CORY                  ASGRS-
VRPVVLETMVGMLNAGITPVVREYGSLGCSGDLAPLSHCALVLMGEGEATDAHG


HUTH_PSEPU                           -
WLSATEALAVAGLEPLTLAAKEGLALLNGTQASTAYALRGLFYAEDLYAAAIACGGLSV
HUTH_RHIME                         -
RMKGDAALKAAGLSPVTLAAKEGLALINGTQVSTALALAGLFRAHRAGQAALITGALST
HUTH_MOUSE
GWADAKYVLEAHGLKPIVLKPKEGLALINGTQMITSLGCEALERASAIARQADIVAALTL
HUTH_RAT
GWADAKYVLEAHGLKPIVLKPKEGLALINGTQMITSLGCEAVERASAIARQADIVAALTL
HUTH_HUMAN
GWADAKYVLEAHGLKPVILKPKEGLALINGTQMITSLGCEAVERASAIARQADIVAALTL
HUTH_CAEEL
GWQPADVVLKKNNLEPLELGPKEGLALINGTQMVTALGAYTLERAHNIARQADVIAALSL
HUTH_BACS                         -
RMPAMTGLKKAGIQPVTLTSKEGLALINGTQAMTAMGVVAYIEAEKLAYQTERIASLTI
HUTH_STRGR
TVRPAGELLAAHGIAPVELREKEGLALLNGTDGMLGMLVMALADLRNLYTSADITAALSL
HUTH_CORY
DIRPVPELFAEAGLTPVELAEKEGLALVNGTDGMLGQLIMALADLDELLDIADATAAMSV
```

Figure 13 cont'd.

```
HUTH_PSEPU        EAVLGSRSPFDARIHE-ARGQRGQIDTAACFRDLLGDSSEVSLSHKNCD----
KVQDPYS
HUTH_RHIME        DAAMGSSAPFHPDIQH-CAAIRARSTRAAALRQLLTG-SPIRQSHIEGDE---
RVQDPYC
HUTH_MOUSE        EVLKGTTKAFDTDIHA-VRPHRGQIEVAFRFRSLLDS-
DHHPSEIAESHRFCDRVQDAYT
HUTH_RAT          EVLKGTTKAFDTDIHA-VRPHRGQIEVAFRFRSLLDS-
DHHPSEIAESHRFCDRVQDAYT
HUTH_HUMAN        EVLKGTTKAFDTDIHA-LRPHRGQIEVAFRFRSLLDS-
DHHPSEIAESHRFCDRVQDAYT
HUTH_CAEEL        DVLKGTTRAYDPDIHR-IRPHRGQNLSALRLRALLHS-
EANPSQIAESHRNCTKVQDAYT
HUTH_BACS         EGLQGIIDAFDEDIHL-ARGYQEQIDVAERIRFYLSD-SGLTTSQGE-----
LRVQDAYS
HUTH_STRGR        EALLGTDKVLAPELHA-IRPHPGQGVSADNMSRVLAG-SGLTGHHQDDAP---
RVQDAYS
HUTH_CORY         EAQLGTDQVFRAELHEPLRPHPGQGRSAQNMFAFLAD-SPIVASHREGDG---
RVQDAYS


HUTH_PSEPU
LRCQPQVMGACLTQLRQAAEVLGIEANAVSDNPLVFAAEGDVISGGNFHAEPVAMAADNL
HUTH_RHIME        IRCQPQVDGACLDLLRSVAATLTIEANAVTDNPLVLSDN-
SVVSGGNFHAEPVAFAADQI
HUTH_MOUSE
LRCCPQVHGVVNDTIAFVKDIITTELNSATDNPMVFASRGETISGGNFHGEYPAKALDYL
HUTH_RAT
LRCCPQVHGVVNDTIAFVKDIITTELNSATDNPMVFASRGETISGGNFHGEYPAKALDYL
HUTH_HUMAN
LRCCPQVHGVVNDTIAFVKNIITTELNSATDNPMVFANRGETVSGGNFHGEYPAKALDYL
HUTH_CAEEL
LRCVPQVHGVVHDTIEFVREIITTEMNSATDNPLVFADREEIISGGNFHGEYPAKALDFL
HUTH_BACS
LRCIPQVHGATWQTLGYVKEKLEIEMNAATDNPLIFNDGDKVISGGNFHGQPIAFAMDFL
HUTH_STRGR        VRCAPQVNGAGRDTLDHAALVAGRELASSVDNPVVLPDG-
RVESNGNFHGAPVAYVLDFL
HUTH_CORY         LRCSPQVTGAARDTIAHARLVATRELAAAIDNPVVLPSG-
EVTSNGNFHGAPVAYVLDFL


HUTH_PSEPU        ALAIAEIGSLSERRISLMMDKHMS-
QLPPFLVENGGVNSGFMIAQVTAAALASENKALSH
HUTH_RHIME
ALAVCEIGAISQRRIALLVDPALSLRLPAFLAKKPGLNSGLMIAEVTSAALMSENKQLSH
HUTH_MOUSE        AIGVHELAAISERRIERLCNPSLS-
ELPAFLVAEGGLNSGFMIAHCTAAALVSESKALCH
HUTH_RAT          AIGVHELAAISERRIERLCNPSLS-
ELPAFLVAEGGLNSGFMIAHCTAAALVSESKALCH
HUTH_HUMAN        AIGIHELAAISERRIERLCNPSLS-
ELPAFLVAEGGLNSGFMIAHCTAAALVSENKALCH
HUTH_CAEEL        AIAVAELAQMSERRLERLVNKELS-
GLPTFLTPDGGLNSGFMTVQLCAASLVSENKVLCH
HUTH_BACS         KIAISELANIAERRIERLVNPQLN-
DLPPFLSPHPGLQSGAMIMQYAAASLVSENKTLAH
HUTH_STRGR
AIVAADLGSICERRTDRLLDKNRSHGLPPFLADDAGVDSGLMIAQYTQAALVSEMKRLAV
HUTH_CORY
AIAVADLGSIAERRTDRMLDPARSRDLPAFLADDPGVDSGMMIAQYTQAGLVAENKRLAV
```

Figure 13 cont'd.

```
HUTH_PSEPU        PHSVDSLPTSANQEDHVSMAPAAGKRLWEMAENTRGVPAIEWLGACQGLDLRKG—LKTS
HUTH_RHIME        PASVDSTPTSANQEDHVSMACHGARRLLQMTENLFSIIGIEALAAVQGIEFRAP—LTTS
HUTH_MOUSE        PSSVDSLSTSAATEDHVSMGGWAARKALRVVEHVEQVLAIELLAACQGIEFLRP—LKTT
HUTH_RAT          PSSVDSLSTSAATEDHVSMGGWAARKALRVIEHVEQVLAIELLAACQGIEFLRP—LKTT
HUTH_HUMAN        PSSVDSLSTSAATEDHVSMGGWAARKALRVIEHVEQVLAIELLAACQGIEFLRP—LKTT
HUTH_CAEEL        PSSVDSIPTSCNQEDHVSMGGFAARKALTVVEHVEAVLAMELLAACQGIEFLKP—LIST
HUTH_BACS         PASVDSIPSSANQEDHVSMGTIAARHAYQVIANTRRVIAIEAICALQAVEYRGI—EHAA
HUTH_STRGR
PASADSIPSSAMQEDHVSMGWSAARKLRTAVDNLARIVAVELYAATRAIELRAAEGLTPA
HUTH_CORY         PA-VDSIPSSAMQEDHVSLGWHAARKLPTSVANLRRILAVEMLIAGRALDLRAP—LKPG


HUTH_PSEPU        AKLEKARQALRSEVA-HYDRDRFFAPDIEKAVELLAKG---S-LTGLLPAGVLPSL---
-
HUTH_RHIME        PELQKAAAAVRGVSS-SIEEDRYMADDLKAAGDLVASG---R-LAAAVSAGILPKLEN—
HUTH_MOUSE        TPLEKVYDLVRSVVR-
PWIKDRFMAPDIEAAHRLLLDQKVWEVAAPYIEKYRMEHIPESR
HUTH_RAT          TPLEKVYDLVRSVVR-
PWIKDRFMAPDIEAAHRLLLDQKVWEVAAPYIEKYRMEHIPESR
HUTH_HUMAN        TPLEKVYDLVRSVVR-
PWIKDRFMAPDIEAAHRLLLEQKVWEVAAPYIEKYRMEHIPESR
HUTH_CAEEL        APLHKIYQLVRSVAP-
PLNEDRYMKPEIDAVLEMIRENRIWEAVLPHLETLEAMEELDPD
HUTH_BACS         SYTKQLFQEMRKVVP-SIQQDRVFSYDIERLTDWLKK----ESLIPDHQNKELRGMNI-
HUTH_STRGR        PASEAVVAALRAAGAEGPGPDRFLAPDLAAADTFVREG---R-LVAAVEPVTGPLA---
-
HUTH_CORY         PATGAVLEVLRSKVA-GPGQDRFLSAELEAAYDLLANG---S-VHKALEAHLPE-----
-



HUTH_PSEPU        ------------------------------
HUTH_RHIME        ------------------------------
HUTH_MOUSE        PLSPTAFSLESLRKNSATIPESDDL----
HUTH_RAT          PLSPTAFSLESLRKNSATIPESDDL----
HUTH_HUMAN        PLSPTAFSLQFLHKKSTKIPESEDL----
HUTH_CAEEL        ALRQFTKTPTGIVQDRSMIPISDDEESIE
HUTH_BACS         ------------------------------
HUTH_STRGR        ------------------------------
HUTH_CORY         ------------------------------
```

Figure 14


```
                                                           1                                                                                                        80
  983831            100.0%   [ MASAPQITLGLSGATADDVIAVARHEARISISPQVLEELASVRAHIDALASADTPVYGISTGFGALATRHIAPEDRAKLQ
 1 SWALL:CAC21618     66.1%   ---MHTVVVGTSGVTASDVLAVARAGARIELSEEAVAALAAARSVVDALAAKPDPVYGVSTGFGALATRHISPELRGRLQ
 2 SWALL:HUTH_STRGR   65.4%   -MDMHTVVVGTSGTTAEDVVAVARHGARVELSAAAVEALAAARLIVDALAAKPEPVYGVSTGFGALASRHIGTELRAQLQ
 3 SWALL:HUTH_DEIRA   46.8%   ----MILDRDLNLEQFISVRHGEQVELSAAARERIARARTVIEQIVEGDTPIYGVNTGFGKFENVQIDRSQLAQLQ
 4 SWALL:BAB16159     42.0%   -------VPLHHLADIYWNNGSAKLDPSFDAAVLKGAARIAEIAAGNAPVYGINTGFGKLASIKIDAADLATLQ
 5 SWALL:Q9KWE4       42.0%   -------VPLHHLADIYWNNGSAKLDPSFDAAVLKGAARIAEIAAGNAPVYGINTGFGKLASIKIDAADLATLQ
 6 SWALL:HUTH_BACSU   40.4%   ----MVTLDGSSLTTADVARVLFDFEEAAASEESMERVKKSRAAVERIVRDEKTIYGINTGFGKFSDVLIQKEDSAALQ
 7 SWALL:Q9KSQ4       42.2%   ---MLHLMIKPGQLSLKQLRQVSRSPVVLSLDPEAIPAIAESAQVVEQVISEGRTVYGINTGFGLLANTKIAPQDLETLQ
 8 SWALL:Q9HU85       41.7%   ----MSLHLKPGQLTLADLRQAYLAPVRLSLDPSADAPIAASVACVENIIAEGRTAYGINTGFGLLASTRISPADLEKLQ
 9 SWALL:Q9KBE6       39.3%   --MTNLKLLDGRSLSLHDLHRIIYEGETVGASDESMEKVKQSRKAVEQIVADEKIIYGITTGFGKFSDIFIDPDDVENLQ
10 SWALL:HUTH_PSEPU   41.7%   ---TELTLKPGTLTLAQLRAIHAAPVRLQLDASAAPAIDASVACVEQIIAEDRTAYGINTGFGLLASTRIASHDLENLQ
11 SWALL:HUTH_RHIME   40.6%   ------LRPGSVPLSDLETIYWTGAPARLDAAFDAGIAKAAARIAEIVAGNAPVYGINTGFGKLASIKIDSSDVATLQ
12 SWALL:Q9HU90       40.7%   MSDLPSVVFGDGPLRWQELVAVARHGARLELSAAAWARIDNARAIVCRIVANGERAYGISTGLGALCDVLLEGEQLAELS
13 SWALL:HUTH_HUMAN   39.2%   KYREPEKYIELDGLTTEDLVNLGKGRYKIKLTPTAEKRVQKSREVIDSIIKEKTVVYGITTGFKFA-RTVIPINKLQLQ
14 SWALL:HUTH_CAEEL   38.8%   VLAPPTKLLILDGNSPEDLVRCEKGECAIQLSMESEDRIRKARTFLEKIASEHRAVYGVTTGFTFSNVTIPPEKLKKLQ
15 SWALL:Q9HLI6       41.0%   ----MIEIDGRSLRVEDVYAVAVEYDRVSISDDTLKAVEEKHEAFLKLINSGKTVYGVNTGFGSLLNVHIERDQEIELQ
16 SWALL:HUTH_MOUSE   38.6%   KYREPEKYIALDGDSTEDLVNLGKGRYKIKLTSIAEKKVQQSREVIDSIIKERTVVYGITTGFKFA-RTVIPANKLQLQ
17 SWALL:BAB29407     38.6%   KYREPEKYIALDGDSTEDLVNLGKGRYKIKLTSIAEKKVQQSREVIDSIIKERTVVYGITTGFKFA-RTVIPANKLQLQ
18 SWALL:HUTH_RAT     38.2%   KYREPEKYIALDGDSTEDLVNLGKGHYKIKLTSIAEKKVQQSREVIDSIIKERTVVYGITTGFKFA-RTVIPANKLQLQ
19 SWALL:AAG53586     39.8%   ---MNALTLTPGTLTLAQLRQVWQQPLQLTLDESAHEAINDSVACVEAIVAEGRTAYGINTGFGLLAQTRIATHDLENLQ
20 SWALL:Q9KKE0       38.9%   ----MGEMISLDGPLTWREIASIAEGASLDLSGPARLRIAQARRIVDALVERGIRGYGINTGVGALCDVIISRENQQALS
21 SWALL:Q9HQD5       42.2%   ------------MSDTRIDAADREALQ
```

Figure 14, cont'd.

```
                          81                                                                            160
                      100.0%  [                 .                   .         .          :          .
983831                100.0%   RSLIRSHAAGMGEPVEREVVRALMFLRAKTLASGRTGVRPVVLETMVGMLNAGITPVVREYGSLGCSGDLAPLSHCALVL
1  SWALL:CAC21618      66.1%   RNIVRSHAAGMGPRVEREVVRALMFLRLKTVCSGRTGVRPEVAQTMADVLNAGITPVVHEYGSLGCSGDLAPLSHCALTL
2  SWALL:HUTH_STRGR    65.4%   RNIVRSHAAGMGPRVEREVVRALMFLRLKTVASGHTGVRPEVAQTMADVLNAGITPVVHEYGSLGCSGDLAPLSHCALTL
3  SWALL:HUTH_DEIRA    46.8%   HNLIVSHAIGMGEPLPAEVVRGMLLLRAQSLSLGHSGVRVEVELLLALLNADALPVVPSQGSVGASGDLAPLAHLALGL
4  SWALL:BAB16159      42.0%   RNLILSHCCGVGAPLPENVVRLIMALKLISLGRGASGVRIELIRLIEGMLEKGVIPVIPEKGSVGASGDLAPLAHMSATM
5  SWALL:Q9KWE4        42.0%   RNLILSHCCGVGAPLPENVVRLIMALKLISLGRGASGVRIELIRLIEGMLEKGVIPVIPEKGSVGASGDLAPLAHMSATM
6  SWALL:HUTH_BACSU    40.4%   LNLILSHACGVGDPFPECVSRAMLLLRANALLKGFSGVRAELIEQLLAFLNKRVHPVIPQQGSLGASGDLAPLSHLALAL
7  SWALL:Q9KSQ4        42.2%   KSIVLSHAAGIGELMSDETVRLMMLLKINSLARGYSGIRLEVIQALIELVNNQIYPCVPKKGSVGASGDLAPLAHMSTVL
8  SWALL:Q9HU85        41.7%   RSIVLSHAAGVGEALDDAMVRLVMLLKVNSLARGFSGIRRKVIDALIALINAEVYPHIPLKGSVGASGDLAPLAHMSLVL
9  SWALL:Q9KBE6        39.3%   HNLIYSHACGVGSPFPETVSRTMLVLRANALLKGFSGVRPLVIERLLALVNANIHPVIPQQGSLGASGDLAPLSHLALVL
10 SWALL:HUTH_PSEPU    41.7%   RSLVLSHAAGIGAPLDDDLVRLIMVLKINSLSRGFSGIRRKVIDALIALVNAEVYPHIPLKGSVGASGDLAPLAHMSLVL
11 SWALL:HUTH_RHIME    40.6%   RNLILSHCCGVGQPLTEDIVRLIMALKLISLGRGASGVRLELVRLIEAMLDKGVIPLIPEKGSVGASGDLAPLAHMAAVM
12 SWALL:Q9HU90        40.7%   RNTLLSHACGVGEPLRDEQTRAIICAAVANYSQGKSGLDRSLVEGLLALLNHGITPQVPAQGSVGY---LTHMAHVGIAL
13 SWALL:HUTH_HUMAN    39.2%   VNLVRSHSSGVGKPLSPERCRMLLALRINVLAKGYSGISLETLKQVIEMFNASCLPYVPEKGTVGASGDLAPLSHLALGL
14 SWALL:HUTH_CAEEL    38.8%   LNLIRSHATGYGEPLAPNRARMLLALRINILAKGHSGISVENIKKMIAAFNAFCVSYVPQQGTVGCSGDLCPLAHLALGL
15 SWALL:Q9HLI6        41.0%   KNLIRSHSSGVGDYLENRYVRAIMAVRLNSLAAGYSAVSADLLNMMVEMLNRDVIPAVPKYGSVGASGDLAPLAHIGLAM
16 SWALL:HUTH_MOUSE    38.6%   VNLVRSHSSGVGKPLSPERCRMLLALRINVLAKGYSGISLETLKQVIEAFNASCLSYVPEKGTVGASGDLAPLSHLALGL
17 SWALL:BAB29407      38.6%   VNLVRSHSSGVGKPLSPERCRMLLALRINVLAKGYSGISLETLKQVIEAFNASCLSYVPEKGTVGASGDLAPLSHLALGL
18 SWALL:HUTH_RAT      38.2%   VNLVRSHSSGVGKPLSPERCRMLLALRINVLAKGYSGISLETLKQVIEVFNASCLSYVPEKGTVGASGDLAPLSHLALGL
19 SWALL:AAG53586      39.8%   RSLVLSHAAGVGEPLDDDIVRLMMVLKINSLARGFSGIRLSVIQALIALVNAGVYSVDPAKGSVGASGDLAPLAHMSLTL
20 SWALL:Q9KKE0        38.9%   RNIILSHACGVGDPLGRVEARAVMAAQIANLTHGYSGVRVETAEMLLALLNADIIPLIPSRGSVGY-----LTHAALVL
21 SWALL:Q9HQD5        42.2%   ANLVRSHAAGAGSELDTAAVRALLVTRLNALAKGYSGIRERVLDVLVGLLNEGVHPVVPSRGSLGASGDLAPLAHMSRVL
```

Figure 14, cont'd.

FIGURE 14

```
                 161                                                                      . 240
[                 .                             .            2            .            .
   983831      100.0%  MGEGEATDAHGDIRPVPELFAEAGLTPVELAEKEGLALVNGTDGMLGQLIMALADLDELLDIADATAAMSVEAQLGTDQV
 1 SWALL:CAC21618    66.1%  MGEGDAEGPDGTVRPAGELLAAHGIAPVELREKEGLALLNGTDGMLGMLVMALADLDTLYKSADITAALTMEALLGTDRV
 2 SWALL:HUTH_STRGR  65.4%  MGEGEAEGPDGTVRPAGELLAAHGIAPVELREKEGLALLNGTDGMLGMLVMALADLRNLYTSADITAALSLEALLGTDKV
 3 SWALL:HUTH_DEIRA  46.8%  IGLGDI-EYQGQVRPAADVLAELGLSPVQLQAKEGLALINGTQLMGSLLALALHDAQVLLGTANLAAAMTVEARYGSHRP
 4 SWALL:BAB16159    42.0%  MGEGEAF-YQGVQMPSKDALAKAGLSPVVLAAKEGLALINGTQTSTALALAGLFRAHRAAQSALVTGALSTDAAMGSSAP
 5 SWALL:Q9KWE4      42.0%  MGEGEAF-YQGVQMPSKDALAKAGLSPVVLAAKEGLALINGTQTSTALALAGLFRAHRAAQSALVTGALSTDAAMGSSAP
 6 SWALL:HUTH_BACSU  40.4%  IGQGEVF-FEGERMPAMTGLKKAGIQPVTLTSKEGLALINGTQAMTAMGVVAYIEAEKLAYQTERIASLTIEGLQGIIDA
 7 SWALL:Q9KSQ4      42.2%  LGEGQAR-YNGKIISGLEAMKIAGLEPITLAPKEGLALLNGTQASTAFALEGLFVAEDLFASATVCGAMSVEAALGSRRP
 8 SWALL:Q9HU85      41.7%  IGESRARH-RGEWLPAAEALAVAGLEPLTLAAKEGLALINGTQVSTAYALRGLFEAEDLFAAATVCGGLSVEAMLGSRAP
 9 SWALL:Q9KBE6      39.3%  LGEGEVF-YKGTKTKASFALKEEIEPITLTAKEGLALINGTQAMTAMGVIAYLEAEKLAFQSEIIASLTMEGLRGIIDA
10 SWALL:HUTH_PSEPU  41.7%  LGEGKAR-YKGQWLSATEALAVAGLEPLTLAAKEGLALINGTQASTAYALRGLFYAEDLYAAAIACGGLSVEAVLGSRSP
11 SWALL:HUTH_RHIME  40.6%  MGHGEAFFAGERMKGDAALKA-AGLSPVTLAAKEGLALINGTQVSTALALAGLFRAHRAGQAALITGALSTDAAMGSSAP
12 SWALL:Q9HU90      40.7%  LGIGEVS-YRGSVVPAAAALAAEGLATVRLGAKDGLCLVNGTPCMTGLACLALDDAQRLAQWADVIGAMSFEALRGQLAA
13 SWALL:HUTH_HUMAN  39.2%  VGEGKMWSPKSGWADAKYVLEAHGLKPVILKPKEGLALINGTQMITSLGCEAVERASAIARQADIVAALTLEVLKGTTKA
14 SWALL:HUTH_CAEEL  38.8%  LGEGKMWSPTTGWQPADVVLKKNNLEPLELGPKEGLALINGTQMVTALGAYTLERAHNIARQADIVAALSLDVLKGTTRA
15 SWALL:Q9HLI6      41.0%  MGEGKAF-FEGRLMDSARALEKAGLKPYQFKEKEGVALINGTSFMSGILSIAVMDAHDILENAIRSALLSFEALGGTSKA
16 SWALL:HUTH_MOUSE  38.6%  IGEGKMWSPKSGWADAKYVLEAHGLKPIVLKPKEGLALINGTQMITSLGCEALERASAIARQADIVAALTLEVLKGTTKA
17 SWALL:BAB29407    38.6%  IGEGKMWSPKSGWADAKYVLEAHGLKPIVLKPKEGLALINGTQMITSLGCEALERASAIARQADIVAALTLEVLKGTTKA
18 SWALL:HUTH_RAT    38.2%  IGEGKMWSPKSGWADAKYVLEAHGLKPIVLKPKEGLALINGTQMITSLGCEAVERASAIARQADIVAALTLEVLKGTTKA
19 SWALL:AAG53586    39.8%  LGEGKAR-YRGEWLPAATALQKAGLAPVTLAAKEGLALLNGTQASTAFALRGLFEAEDLFASAVVCGALTTEAVLGSRRP
20 SWALL:Q9KKE0      38.9%  IGHGSAMQGTERLSGADAL-ARLGLAPLRLEAKEGLSLVNGTPCATGLAALALARTERLFAWADAAAAMTYE-NLGSQAN
21 SWALL:Q9HQD5      42.2%  IGEGQA-DVAGERMPAAEALAAADLEPVTLQAKEGLALINGTQLTTGVAALALVDAERVLRSADTAGALTTEVTMSTTAS
```

Figure 14, cont'd.

```
                                   241                                                                                      320
                                          .         .         .         .         .         .         .         .
                                                                          3                                             320
        983831             100.0%  FRAELHEPLRPHPGQGRSAQNMFAFLADSPIVASHREGDGRVQDAYSLRCSPQVTGAARDTIAHARLVATRELAAAIDNP
 1  SWALL:CAC21618          66.1%  LAPELHA-IRPHPGQAASAANMAAVLKGSGLTGHHQDDAPRVQDAYSVRCAPQVAGAGRDTMAHAGLVAERELAAAVDNP
 2  SWALL:HUTH_STRGR        65.4%  LAPELHA-IRPHPGQGVSADNMSRVLAGSGLTGHHQDDAPRVQDAYSVRCAPQVNGAGRDTLDHAALVAGRELASSVDNP
 3  SWALL:HUTH_DEIRA        46.8%  FQPDV-VGLRPHPGALAVAAELREFLAGSEIAPSHLTGDGKVQDAYSLRAVPQVHGATWDALAQAERVLAVEFASVTDNP
 4  SWALL:BAB16159          42.0%  FHPDIHT-LRGHKGQIDAGSALRNLLQGSEIRESHIEGDERVQDPYCIRCQPQVDGACLDLLASVARTLEIEANAVTDNP
 5  SWALL:Q9KWE4            42.0%  FHPDIHT-LRGHKGQIDAGSALRNLLQGSEIRESHIEGDERVQDPYCIRCQPQVDGACLDLLASVARTLEIEANAVTDNP
 6  SWALL:HUTH_BACSU        40.4%  FDEDIHLA-RGYQEQIDVAERIRFYLSDSGLTTS--QGELRVQDAYSLRCIPQVHGATWQTLGYVKEKLEIEMNAATDNP
 7  SWALL:Q9KSQ4            42.2%  FDPRIHR-VRGHRTQMDAATAYRHLLVSSEIGQSHSNCE-KVQDPYSLRCQPQVMGACLQQIRSAAEVLEVEANSVSDNP
 8  SWALL:Q9HU35            41.7%  FDARIHAA-RGQRGQIDVAAAYRDLLASSEVARSHEKCD-KVQDPYSLRCQPQVMGACLTQMRQAAEVLEIEANAVSDNP
 9  SWALL:Q9KBE6            39.3%  FDEQIHFA-RGYVEQVDVARRMESYLQDSQLTT--RQGELRVQDAYSLRCIPQVHGATWQTLRYVKEKLEIEMNAATDNP
10  SWALL:HUTH_PSEPU        41.7%  FDARIHEA-RGQRGQIDTAACFRDLLGDSSEVSSHKNCD-KVQDPYSLRCQPQVMGACLTQLRQAAEVLGIEANAVSDNP
11  SWALL:HUTH_RHIME        40.6%  FHPDIQHCAAIRARSTRAAA-LRQLLTGSPIRQSHIEGDERVQDPYCIRCQPQVDGACLDLLRSVAATLTIEANAVTDNP
12  SWALL:Q9HU90            40.7%  FDAEI-VALKPHPGMQRVAANLRALLAGSQVLENAR--GIRTQDALSIRSIPQIHGACRDQLAHARQIET-ELNSATDNP
13  SWALL:HUTH_HUMAN        39.2%  FDTDIHA-LRPHRGQIEVAFRFRSLLSDSEIAESHRFCD-RVQDAYTLRCCPQVHGVVNDTIAFVKNIITTELNSATDNP
14  SWALL:HUTH_CAEEL        38.8%  YDPDIHR-IRPHRGQNLSALRLRALLNPSQIAESHRNCT-KVQDAYTLRCVPQVHGVVHDTIEFVREIITTEMNSATDNP
15  SWALL:Q9HLI6            41.0%  FTPWILGA-RPHLGQVAIGNRFREYLTGSDIV--KRADSVKVQDAYTLRCIPQVYGSVADVIDYVENVLSVEINSATDNP
16  SWALL:HUTH_MOUSE        38.6%  FDTDIHA-VRPHRGQIEVAFRFRSLLSDSEIAESHRFCD-RVQDAYTLRCCPQVHGVVNDTIAFVKDIITTELNSATDNP
17  SWALL:BAB29407          38.6%  FDTDIHA-VRPHRGQIEVAFRFRSLLSDSEIAESHRFCD-RVQDAYTLRCCPQVHGVVNDTIAFVKDIITTELNSATDNP
18  SWALL:HUTH_RAT          38.2%  FDTDIHA-VRPHRGQIEVAFRFRSLLSDSEIAESHRFCD-RVQDAYTLRCCPQVHGVVNDTIAFVKDIITTELNSATDNP
19  SWALL:AAG53586          39.8%  FDARIHE-VRGQRGQIDAAALFRHVLTDTSAIASHHNCD-KVQDPYSLRCQPQVMGACLTQMRQVAEVLLVESNAVSDNP
20  SWALL:Q9KKE0            38.9%  AFAELPLALRQSPGLSAVGEGLRDWLADSPMLAG--TAGTRTQDPLSLRAVPQVHGAARDAFGQVAEIVDRELASVTDNP
21  SWALL:Q9HQD5            42.2%  CAPAIHE-VRPHDGQAVSARHIRNLTAGSEVLDHHRDCD-RVQDAYSIRCLPQVHGAVRDALDHLRAAVATELNSATDNP
```

Figure 14, cont'd.

```
                          321                                                                                          400
                          [                               .                   :                   .                   .      ]
983831            100.0%  VVLPSGEVTSNGNFHGAPVAYVLDFLAIAVADLGSIAERRTDRMLDPARSRDLPAFLADDPGVDSGMMIAQYTQAGLVAE
 1 SWALL:CAC21618  66.1%  VVLPDGRVESNGNFHGAPVAYVLDFLAVAVADLGSIAERRTDRLLDKNRSHGLPPFLADDAGVDSGLMIAQYTQAALVGE
 2 SWALL:HUTH_STRGR 65.4%  VVLPDGRVESNGNFHGAPVAYVLDFLAIVADLGSICERRTDRLLDKNRSHGLPPFLADDAGVDSGLMIAQYTQAALVSE
 3 SWALL:HUTH_DEIRA 46.8%  LIFPTGEVVSGGNFHGQPLAVTIDALKVAVAELGSISERRTEQLLNPALS-GLPAFLTPNGGLNSGFMIAQYTSAALVSE
 4 SWALL:BAB16159   42.0%  LVLSDNSVVSGGNFHAEPVAFAADQTALAVCEIGAIAQRRIALLVDPALSYGLPAFLSKKPGLNSGLMIAEVTSAALMSE
 5 SWALL:Q9KWE4     42.0%  LVLSDNSVVSGGNFHAEPVAFAADQTALAVCEIGAIAQRRIALLVDPALSYGLPAFLSKKPGLNSGLMIAEVTSAALMSE
 6 SWALL:HUTH_BACSU 40.4%  LIENDGDVISGGNFHGQPIAFAMDFLKIAISELANIAERRIERLVNPQLN-DLPPFLSPHPGLQSGAMIMQYAAASLVSE
 7 SWALL:Q9KSQ4     42.2%  LVFADGDIISGGNFHAEPVAMAADNLALAIAEIGSLSERRMALLIDSALSK-LPPFLVDNGGVNSGFMIAQVTAAALASE
 8 SWALL:Q9HU85     41.7%  LVFAAGDVISGGNFHAEPVAMAADNLALALAEIGSLSERRISLMMDMHMSQ-LPPFLVANGGVNSGFMIAQVTAAALASD
 9 SWALL:Q9KBE6     39.3%  LIFDNGQVISGGNFHGQQIALAMDFLGIAMAELANISERRIERLVNPQLN-DLPPFLSAAPGVQSGVMILQYCAASLVSE
10 SWALL:HUTH_PSEPU 41.7%  LVFAAGDVISGGNFHAEPVAMAADNLALAIAEIGSLSERRISLMMDKHMSQ-LPPFLVENGGVNSGFMIAQVTAAALASE
11 SWALL:HUTH_RHIME 40.6%  LVLSDNSVVSGGNFHAEPVAFAADQIALAVCEIGAISQRRIALLVDPALSLRLPAFLAKKPGLNSGLMIAEVTSAALMSE
12 SWALL:Q9HU90     40.7%  LLLGTPEVVSQANPHGESVAMAADLLAIAVAELGGVAERRLDRLVNPLVS-GLPAFLVGKPGVNSGMMITQYVAASLAGE
13 SWALL:HUTH_HUMAN 39.2%  MVFANGETVSGGNFHGEYPAKALDYLAIGIHELAAISERRIERLCNPSLS-ELPAFLVAEGGLNSGFMIAHCTAAAIVSE
14 SWALL:HUTH_CAEEL 38.8%  LVFADREIISGGNFHGEYPAKALDFLAIAVAELAQMSERRLERLVNKELS-GLPTFLTPDGGLNSGFMTVQLCAASLVSE
15 SWALL:Q9HLI6     41.0%  L-FNGEEVVSGGNFHGEPVALAADFLAIAILTDLGNMVERRIARLVDTNLS-GLPPFLTPDSGLNSGYMIPQYTAAALCNR
16 SWALL:HUTH_MOUSE 38.6%  MVFASGETISGGNFHGEYPAKALDYLAIGVHELAAISERRIERLCNPSLS-ELPAFLVAEGGLNSGFMIAHCTAAAIVSE
17 SWALL:BAB29407   38.6%  MVFASGETISGGNFHGEYPAKALDYLAIGVHELAAISERRIERLCNPSLS-ELPAFLVAEGGLNSGFMIAHCTAAAIVSE
18 SWALL:HUTH_RAT   38.2%  MVFASGETISGGNFHGEYPAKALDYLAIGVHELAAISERRIERLCNPSLS-ELPAFLVAEGGLNSGFMIAHCTAAAIVSE
19 SWALL:AAG53586   39.8%  LVFAANEMVFRGNFHAEPVAMAADNLALAIAEIGALSERRIALMMDKHMSQ-LPPFLVRNGGVNSGFMIAQVTAAALASE
20 SWALL:Q9KKE0     38.9%  AVAGSPEVHSQAHAVGAALGLAMDSLAVAVAEVAAISERRIDRLVNPLVS-GLPAFLAGDSGVSSGFMIAQYTAAALVAE
21 SWALL:Q9HQD5     42.2%  LVFPSGTVVSGGNFHGEVLALRLGYAASALAELAAISERRTDRLLNPETQEPLEPFLAPDSGLHSGLMIPQYTAASLVND
```

Figure 14, cont'd.

```
                          401                                                                                                                                                                       480
983831               100.0%   NKRLAVPASVDSIPSSAMQEDHVSLGWHAARKLRTSVANLRRILAVEMLIAGRALDLRAPLKPGPATGAVLEVLRSKVAG
 1  SWALL:CAC21618     66.1%   LKRLAVPASADSIPSSAMQEDHVSMGWSAARKLRTAVDNLARVIAVELYAATRAIQLREGLTPAPASQAVVEAVRAAVEG
 2  SWALL:HUTH_STRGR    65.4%   MKRLAVPASADSIPSSAMQEDHVSMGWSAARKLRTAVDNLARIVAVELYAATRAIELRAALTPAPASEAVVAALRAAGAG
 3  SWALL:HUTH_DEIRA    46.8%   NKVLSHPASVDSIPTSANQEDHVSMGAHAARQLRQIVANVQTVLSIELLCAAQGLDFQQ-LRAGRGVQAAYEYVRTFVPT
 4  SWALL:BAB16159      42.0%   NKQMSHPASVDSTPTSANQEDHVSMACHGARRLLAMTDNLFGILGIEALAAVQGVELRGPLKTSPELEKAAAVLRSAVPV
 5  SWALL:Q9KWE4        42.0%   NKQMSHPASVDSTPTSANQEDHVSMACHGARRLLAMTDNLFGILGIEALAAVQGVELRGPLKTSPELEKAAAVLRSAVPV
 6  SWALL:HUTH_BACSU    40.4%   NKTLAHPASVDSIPSSANQEDHVSMGTIAARHAYQVIANTRRVIAIEAICALQAVEYRGIEHAASYTKQLFQEMRKVVPS
 7  SWALL:Q9KSQ4        42.2%   NKTLAHPASVDSLPTSANQEDHVSMATFAARRLRDMGENTRGILAVEYLAAAQGLDFRAPLKSSPRIEEARQILREKVPF
 8  SWALL:Q9HU85        41.7%   NKALAHPASVDSLPTSANQEDHVSMGTIGSRHAYQIIQNVRNVLAIELICAMQAVDIRGREKMASFTKKILEKGREHVPY
 9  SWALL:HUTH_PSEPU    39.3%   NKTLAHPASVDSIPSSANQEDHVSMAPAAGKRLWAMAENVRGILAVEWLGACQGLDFREGLKSSPKLEQARRLLRDKVPY
10  SWALL:HUTH_RHIME    41.7%   NKALSHPHSVDSLPTSANQEDHVSMAPAAGKRLWEMAENTRGVLAIEWLGACQGLDLRKGLKTSAKLEKARQALRSEVAH
11  SWALL:Q9HU90        40.6%   NKQLSHPASVDSTPTSANQEDHVSMACHGARRLLQMTENLFSIIGIEALAAVQGIEFRAPLTTSPELQKAAAAVRGVSSS
12  SWALL:HUTH_HUMAN    40.7%   NRQLAQPAVVDNFVTSALQEDHLSLGTSAALKLGRALENLRRILAIEYLLAAQAFEFLAPQRFGQGTAAAWGILRERVPA
13  SWALL:HUTH_CAEEL    39.2%   NKALCHPSSVDSLSTSAATEDHVSMGGWAARKALTVVEHVEAVLAMELLAACQGIEFLKPLISTAPLHKIYQLVRS-VAP
14  SWALL:Q9HLI6        38.8%   NKVLCHPSSVDSIPTSCNQEDHVSMGATGSLKLLEIIDNVRYIIAIEYLLGSQALFTDK-GMSPSTRKIYEKIREKVEK
15  SWALL:HUTH_MOUSE    41.0%   NKVLAYPSSADTIPTSANQEDHVSMGGWAARKALRVVEHVEQVLAIELLAACQGIEFLRPLKTTPLEKVYDLVRSVVRP
16  SWALL:BAB29407      38.6%   SKALCHPSSVDSLSTSAATEDHVSMGGWAARKALRVIEHVEQVLAIELLAACQGIEFLRPLKTTPLEKVYDLVRSVVRP
17  SWALL:HUTH_RAT      38.6%   SKALCHPSSVDSLSTSAATEDHVSMGGWAARKALRVIEHVEQVLAVEWLAACQGADLRDGLTSSPLLEQARQSCGEQVAH
18  SWALL:AAG53586      38.2%   SKALCHPSSVDSLSTSAATEDHVSMGGWAARKALRVIEHVEQVLAIELLAAHRPMSCSRKRRARRNAPLPFTGTYARRSP
19  SWALL:Q9KKE0        39.8%   NKGLCHPTSVDK-PPSANQEDHVSMAPAAGRRLWEMAGNTRGVLAVEWLAACQGADLRDGLTSSPLLEQARQSCGEQVAH
20  SWALL:Q9HQD5        38.9%   NRRLAAPASLDGGITSALQEDMLTHATPAWKALSIVDNLERILAIELLAAHRPMSCSRKRRARRNAPLPFTGTYARRSP
21                      42.2%   LRSLGQP-TLDNASVSGAQEDHVSMSAGAAYNFREAVEKAATVVGVELLCGAQGREFLDPLALGAGTAAAYDLVR-EVSE
```

Figure 14, cont'd.

```
                          481                   5                  ] 513
983831            100.0%  [  .              .          .
                             PGQDRFLSAELEAAYDLLANGSVHKALEAHLPA ] 513
 1 SWALL:CAC21618   66.1%    PGPDRHLAPDLAAADAFVRAGHLVAAAESVTGP
 2 SWALL:HUTH_STRGR 65.4%    PGPDRFLAPDLAAADTFVREGRLVAAVEPVTGP
 3 SWALL:HUTH_DEIRA 46.8%    LTEDRYFRPDLLRLRGELVSGRVAQAADTQAPA
 4 SWALL:BAB16159   42.0%    LEDDRYMATDLKAAIEVVASGALVSAISSGLPV
 5 SWALL:Q9KWE4     42.0%    LEDDRYMATDLKAAIEVVASGALVSAISSGLPV
 6 SWALL:HUTH_BACSU 40.4%    IQQDRVFSYDIERLTDWLKKESLIPDHQNKELR
 7 SWALL:Q9KSQ4     42.2%    YDKDRYFAPDIEKANALL-QLAVHNRLMPDQLL
 8 SWALL:Q9HU85     41.7%    YQEDRFFAPDIEAASQLLASGCLNALLPARLLP
 9 SWALL:Q9KBE6     39.3%    IDQDRMFAKDIERAAKWLKDGSWDFTKMREKER
10 SWALL:HUTH_PSEPU 41.7%    YDRDRFFAPDIEKAVELLAKGSLTGLLPAGLPS
11 SWALL:HUTH_RHIME 40.6%    IEEDRYMADDLKAAGDLVASGRLAAAVSAGLPK
12 SWALL:Q9HU90     40.7%    YDTDRWLAPDIASAAAILGERKSLARLAASIGD
13 SWALL:HUTH_HUMAN 39.2%    WIKDRFMAPDIEAAHRLLLEQKVWEVAAPYIEK
14 SWALL:HUTH_CAEEL 38.8%    PNEDRYMKPEIDAVLEMIRENRIWEAVLPHLET
15 SWALL:Q9HLI6     41.0%    LDHDRPPSFDIETIRKMMDKKEFISALP-----
16 SWALL:HUTH_MOUSE 38.6%    WIKDRFMAPDIEAAHRLLLDQKVWEVAAPYIEK
17 SWALL:BAB29407   38.6%    WIKDRFMAPDIEAAHRLLLDQKVWEVAAPYIEK
18 SWALL:HUTH_RAT   38.2%    WIKDRFMAPDIEAAHRLLLDQKVWEVAAPYIEK
19 SWALL:AAG53586   39.8%    YDDDRFFAPDIEAAISLLNKGSLVGLLPAFL--
20 SWALL:Q9KKE0     38.9%    PIATIVR--------------------------
21 SWALL:Q9HQD5     42.2%    PAGDRALADDMAAVGDLVRAGLVEDAVARALDA
```

Figure 14, cont'd.

KEY:

983831   : HAL

1	CAC21618	: Streptomyces coelicolor
2	HUTH_STRGR	: Streptomyces griseus
3	HUTH_DEIRA	: Deinococcus radiodurans
4	BAB16159	: Agrobacterium rhizogenes
5	Q9KWE4	: Agrobacterium rhizogenes
6	HUTH_BACSU	: Bacillus subtilis
7	Q9KSQ4	: Vibrio cholerae
8	Q9HU85	: Pseudomonas aeruginosa
9	Q9KBE6	: Bacillus halodurans
10	HUTH_PSEPU	: Pseudomonas putida
11	HUTH_RHIME	: Rhizobium meliloti
12	Q9HU90	: Pseudomonas aeruginosa
13	HUTH_HUMAN	: Human
14	HUTH_CAEEL	: Caenorhabditis elegans
15	Q9HLI6	: Thermoplasma acidophilum
16	HUTH_MOUSE	: Mouse
17	BAB29407	: Mus musculus (Mouse)
18	HUTH_RAT	: Rat
18	AAG53586	: uncultured bacterium pCosAS1
20	Q9KKE0	: Rhizobium meliloti
21	Q9HQD5	: Halobacterium sp

Figure 15

```
STRG    6    VVVGTSGTTAEDVVAVARHGARVELSAAAVEALAAARLIVDALAAKPEPVYGVSTGFGAL
"HAL"   7    ITLGLSGATADDVIAVARHEARISISPQVLEELASVRAHIDALASADTPVYGISTGFGAL
             *    * **  **  **** *       * **      *     **** ***** ****** *

STRG,   66   ASRHIGTELRAQLQRNIVRSHAAGMGPRVEREVVRALMFLRLKTVASGHTGVRPEVAQTM
HAL     67   ATRHIAPEDRAKLQRSLIRSHAAGMGEPVEREVVRALMFLRAKTLASGRTGVRPVVLETM
             * ***        *  * ********* ************* ** *** ****** *  *

STRG    126  ADVLNAGITPVVHEYGSLGCSGDLAPLSHCALTLMGEGEAEGPDGTVRPAGELLAAHGIA
HAL     127  VGMLNAGITPVVREYGSLGCSGDLAPLSHCALVLMGEGEATDAHGDIRPVPELFAEAGLT
               ********** *************************  ******  *  * *   *  *

STRG    186  PVELREKEGLALLNGTDGMLGMLVMALADLRNLYTSADITAALSLEALLGTDKVLAPELH
HAL     187  PVELAEKEGLALVNGTDGMLGQLIMALADLDELLDIADATAAMSVEAQLGTDQVFRAELH
             **** ******* ******** * ******       *    *  **  ****  * ***

STRG    246  A-IRPHPGQGVSADNMSRVLAGSGLTGHHQDDAPRVQDAYSVRCAPQVNGAGRDTLDHAA
HAL     247  EPLRPHPGQGRSAQNMFAFLADSPIVASHREGDGRVQDAYSLRCSPQVTGAARDTIAHAR
               ******* ** **     **           *******  ** ***  * *** * * *

STRG    305  LVAGRELASSVDNPVVLPDGRVESNGNFHGAPVAYVLDFLAIVAADLGSICERRTDRLLD
HAL     307  LVATRELAAAIDNPVVLPSGEVTSNGNFHGAPVAYVLDFLAIAVADLGSIAERRTDRMLD
             *** *****  ******* *  * *************************** ****** **
```

Figure 15, Cont'd.

```
STRG  365  KNRSHGLPPFLADDAGVDSGLMIAQYTQAALVSEMKRLAVPASADSIPSSAMQEDHVSMG
HAL   367  PARSRDLPAFLADDPGVDSGMMIAQYTQAGLVAENKRLAVPASVDSIPSSAMQEDHVSLG
                 *    **** **** ** ********* ***  ********* ****************
                                                                    *

STRG  425  WSAARKLRTAVDNLARIVAVELYAATRAIELRAAEGLTPAPASEAVVAALRAAGAEGPGP
HAL   427  WHAARKLRTSVANLRRILAVEMLIAGRALDLRAP--LKPGPATGAVLEVLRSKVA-GPGQ
           * ******* * ** * *** * *    *** *          **  **  **   *** *

STRG  485  DRFLAPDLAAADTFVREGRLVAAVE
HAL   484  DRFLSAELEAAYDLLANGSVHKALE
           ****   *  *  *         *
```